~~orderable physicochemical property~~ corresponding to said each amino acid in said amino acid sequence of said target polypeptide or protein;

calculating one or more polypeptide eigenvalues and a corresponding polypeptide eigenvector associated with each of said one or more polypeptide eigenvalues by linear decomposition of an autocovariance matrix formed from a sequentially lagged data matrix of said polypeptide physicochemical data series;

ordering said one or more polypeptide eigenvalues and said corresponding polypeptide eigenvectors from largest to smallest;

selecting one or more of said polypeptide eigenvectors;

transforming said one or more of said polypeptide eigenvectors into an eigenvector template;

forming a graph of said eigenvector template, wherein said numerical values ~~of said physicochemical property~~ are graphed along the y-axis of said graph and ordered position in said eigenvector template is graphed along the x-axis of said graph;

partitioning said graph along said y-axis according to said ranges of said numerical values ~~of said physicochemical property~~ defining said peptide constituent groups, to form a plurality of y-axis ranges;

assigning one of said peptide constituents to each position in said peptide or peptide-like molecule by using said graph as a template to create a sequence of a mode-matched peptide, wherein at each ordered position in said eigenvector template along said x-axis of said graph, said one of said peptide constituents assigned to said ordered position has a numerical value ~~of said orderable physicochemical property~~ that is within said y-axis range of said ordered point;

determining a sequence of a retro-inverso peptide by inverting said sequence of a mode-matched peptide; and

synthesizing said retro-inverso peptide from said sequence, using D-amino acids.

2. A method for synthesizing a peptide or a peptide-like molecule based on matching a physicochemical mode of a peptide to the same physicochemical mode of a target polypeptide or protein, followed by synthesizing a retro-inverso version of said peptide comprised of D-amino acids, comprising the steps of:

assigning ~~a numerical value of an orderable physicochemical property~~ to each member of a set of peptide constituents a numerical value representative of the hydrophobic free energy of said each member of a set of peptide constituents, said set of peptide constituents including all the members of the set of naturally-occurring amino acids;

arranging said peptide constituents in order of said numerical values ~~of said orderable physicochemical property~~;

partitioning said set of peptide constituents into a plurality of peptide constituent groups, whereby each of said peptide constituent groups contains at least one member of said set of peptide constituents, each peptide constituent group encompasses a range of said ordered numerical values, and each member of said set of peptide constituents belongs to only one peptide constituent group;

creating a polypeptide physicochemical data series by replacing each amino acid in an amino acid sequence with said numerical value ~~of said orderable physicochemical property~~ corresponding to said each amino acid in said amino acid sequence;

calculating one or more polypeptide eigenvalues and a corresponding polypeptide eigenvector associated with each of said one or more polypeptide eigenvalues by linear decomposition of an autocovariance matrix formed from a sequentially lagged data matrix of said polypeptide physicochemical data series;

ordering said one or more polypeptide eigenvalues and said corresponding polypeptide eigenvectors from largest to smallest;

selecting one or more of said polypeptide eigenvectors;

forming a vector, said vector being a sum of the products of each of said plurality of said polypeptide eigenvectors multiplied by the corresponding eigenvalue;

forming a graph of said vector, wherein said numerical values ~~of said orderable physicochemical property~~ are graphed along the y-axis of said graph, and ordered position in said eigenvector template is graphed along the x-axis of said graph;

partitioning said graph along said y-axis according to said range of said numerical values ~~of said orderable physicochemical property~~ defining said peptide constituent groups, to form a plurality of y-axis ranges; and

assigning one of said peptide constituents to each position in said peptide or peptide-like molecule by using said graph of said vector as a template, wherein at each ordered